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atgagggcccctgctcagatTTTTGGATTCTTGGTCAGGAGACGTTGT  
 1 -----  
 tactcccggggacgagtctaaaaacctaagaaccagtcctctgcaaca  
 ACTAGTCGACATGAGGGCCCCTGCTCAGTTTTTTGGCTTCTTG-3'

A A C AA  
 MKV4 PRIMER

agaaatgagaccgtctattcagttcctggggctcttggttggtctggcttcatgg  
 49 -----  
 tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc

[M R P S I Q F L G L L L F W L H G  
 LEADER

tgctcagtggtgacatccagatgacacagttccatcctcactgtctgcatctct  
 103 -----  
 acgagtcacactgtaggtctactgtgtcagaggtaggagtgacagacgtagaga

A Q C][D I Q M T Q S P S S L S A S L  
 FR1

gggaggcaaagtcaccatcacttgcaagacaagccaagacattaacaagtatat  
 157 -----  
 ccctccggtttcagtggttagtgaacggttctgttcggttctgtaattgttcatata

G G K V T I T C][K T S Q D I N K Y M  
 CDR1

ggcttggtaccaacacaagcctggaaaacgtcctaggctgctcatacattacac  
 211 -----  
 ccgaaccatggttgtgttcggaccttttgcaggatccgacgagtatgtaatgtg

A][W Y Q H K P G K R P R L L I H][Y T  
 FR2

atctgcattacagccaggcatcccatcaaggttcagtggaagtgggtctgggag  
 265 -----  
 tagacgtaatgtcgggtccgtagggttagttccaagtcaccttcacccagaccctc

S A L Q P][G I P S R F S G S G S G R  
 CDR2

FIG. 1-1.

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319 agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta  
 -----  
 tctaataaggaagttgtagtcggttgacctcggacttctataacggttgaataat

D Y S F N I S N L E P E D I A T Y Y  
 FR3

373 ttgtctacagtatgataatctgtggacggttcggtggaggcaccaagctggaaat  
 -----  
 aacagatgtcatactattagacacctgcaagccacctccgtgggttcgaccttta

C][L Q Y D N L W T][F G G G T K L E I  
 CDR3 FR4

MOUSE KAPPA PRIMER

3'-GTAGAAGGGTGGTAGGTGGGCCCT

427 caaacgggctgatgctgcaccaactgtatccatcttcccaccatccacccggga  
 -----  
 gtttgcccgactacgacgtgggttgacataggtagaagggtggtaggtgggcccct

K]

AGG-5'

tcc

481 ---

agg

**FIG. 1-2.**

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atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg  
 1 -----  
 tactttacgtcgacccagtagaagaaggactaccgtcaccaatgtccc  
 ACTAGTCGACATGAAATGCAGCTGGGTCATCTTCTTC-3'

G

MHV1 PRIMER

[M K C S W V M F F L M A V V T G  
 LEADER

gtcaattcagagggttcagctgcagcagctctggggcagagcttgtgaagccaggg  
 49 -----  
 cagttaagtctccaagtcgacgtcgtcagaccccgctctcgaacacttcggtccc

V N S][E V Q L Q Q S G A E L V K P G  
 FR1

gcctcagtcaggttgtcctgcacagcttctggcttcaacattaaagacacctat  
 103 -----  
 cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata

A S V K L S C T A S G F N I K][D T Y  
 CDR1

atacactgtgtgaagcagaggcctgaacagggcctggagtggttggaaggatt  
 157 -----  
 tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa

I H][C V K Q R P E Q G L E W I G][R I  
 FR2

gatcctgcgaatggttataactaaatatgaccggaagttccagggcaaggccact  
 211 -----  
 ctaggacgcttaccaatatgatttataactgggcttcagggtcccgttccggtga

D P A N G Y T K Y D P K F Q G][K A T  
 CDR2

ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca  
 265 -----  
 tattgtcgactgtgtaggagggttgtgtcggatggacgtcgagtcgtcggactgt

I T A D T S S N T A Y L Q L S S L T  
 FR3

FIG. 2-1.

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319 tctgaggacactgccgtctatctgtgctagagagggatattatggtaactac  
-----  
agactcctgtgacggcagataaagacacgatctctccctataataaccattgatg

S E D T A V Y F C A R][E G Y Y G N Y  
CDR3

373 ggggtctatgctatggactactgggggtcaaggaacctcagtcaccgtctcctca  
-----  
ccccagatacagatacctgatgaccccagttccttgaggatcagtggcagaggagt

G V Y A M D Y][W G Q C T S V T V S S]

MOUSE GAMMA-1 PRIMER

3'-GTAGACAGATAGGTGACCGGGCCCTAGG-5

427 gccaaaacgacacccccatctgtctatccactggcccgggatcc  
-----  
cggttttgctgtgggggtagacagataggtgaccgggcccctagg

S S]

**FIG. 2-2.**

09155739-091198

HindIII KOZAK SEQUENCE II/16

1 aagcttgcccgcaccatgagaccgtctattcagttcctggggctcttggtgttc  
 -----  
 ttcgaacggcggtggtactctggcagataagtcaaggacccccgagaacaacaag

[M R P S I Q F L G L L L F  
 LEADER

55 tggcttcatgggtgctcagtgtgacatccagatgacacagtctccatcctcactg  
 -----  
 accgaagtaccacgagtcacactgtaggtctactgtgtcagaggtaggagtgc

W L H G A Q C][D I Q M T Q S P S S L  
 FR1

109 tctgcatctGTAggaGATAGAgtcaccatcacttgcaagacaagccaagacatt  
 -----  
 agacgtagaCATcctCTATCTcagtggtagtgaaacggttctgttcgggttctgtaa

S A S V G D R V T I T C][K T S Q D I  
 CDR1

163 aacaagtatatggcttggtaccaaCAGACacctggaaaaGCTcctaggctgctc  
 -----  
 ttgttcatataccgaaccatgggtGTCTGTggaccttttCGAggatccgacgag

N K Y M A][W Y Q Q T P G K A P R L L  
 FR2

217 atacattacacatctgcattacagccaggcatcccatcaagggttcagtgggaagt  
 -----  
 tatgtaatgtgtagacgtaatgtcgggtccgtagggttagttccaagtcaccttca

I H][Y T S A L Q P][G I P S R F S G S  
 CDR2

271 gggctctgggagagattatACTttcACCatcagcAGCctgCAGcctgaagatatt  
 -----  
 cccagaccctctctaataTGAaagTGGtagtcgTCGgacGTCggacttctataa

G S F R D Y T F T I S S L Q P E D I  
 FR3

FIG. 10-1.

gcaàcttattattgtctacagtatgataatctgtggacgttcggtCAAggcacc  
 325 -----  
 cgttgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg  
 A T Y Y C][L Q Y D N L W T][F G Q G T  
 CDR3 FR4

SPLICE DONOR SITE BamHI  
 aagGTGgaaatcaaacgtgagtggatcc  
 379 -----  
 ttcCACcttttagtttgcactcacctagg

K V E I K]

### FIG. 10-2.

HindIII KOZAK SEQUENCE

AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTTTTGCCTGCTCGCCGTG  
 1 -----  
 TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC

[M D W T W R V F C L L A V  
 LEADER

GCTCCTGGGGCCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG  
 55 -----  
 CGAGGACCCCGGGTGTCTGGTCCACGTTGATCACGTGAGGCCGCGGCTTCACTTC  
 A P G A H S][Q V Q L V Q S G A E V K

AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa  
 109 -----  
 TTTGGGCCACGAAGGCACTTTCAGTCGACATTTTCGATCGCCAaagttgtaattt  
 K P G A S V K V S C K A S G F N I K][  
 FR1

gacacctatatacacTGGGTTAGACAGGCCCCtGGCCAAaGGCTgGAGTGGATg  
 163 -----  
 ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAc  
 D T Y I H][W V R Q A P G Q R L E W M  
 CDR1 FR2

### FIG. 11-1.

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 86T60"6E25T60

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217 G Gaaggattgatcctgcgaatggttataactaaatatgacccgaagttccagggc  
 -----  
 CCttcctaactaggacgccttaccaatatgatttataactgggcttcaagggtccc  
 G][R I D P A N G Y T K Y D P K F Q G][  
 CDR2

271 cgggtcACCatcACCgcaGACACCTCTgccagcACCGCCTACATGGAACTGTCC  
 -----  
 gcccagTGGtagTGGcgtCTGTGGAGAcggtcgTGGCGGATGTACCTTGACAGG  
 R V . T I \_ T A D T S A S T A Y M E L S  
 FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagaggggatattat  
 -----  
 TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata  
 S L R S E D T A V Y Y C A R][E G Y Y

379 ggtaactacgggggtctatgctatgGACTAcTGGGGtCAaGGaACCCTTGTCACC  
 -----  
 ccattgatgccccagatacgatacCTGATgACCCCaGTtCCtTGGGAACAGTGG  
 G N Y G V Y A M D Y][W G Q G T L V T  
 CDR3 FR4

SPLICE DONOR SITE BamHI  
 GTctccTCAGGTGAGTGGATCC  
 433 -----  
 CAGaggAGTCCACTCACCTAGG  
 V S S]

FIG. 11-2.